

Resource Summary Report

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InterEvol database

RRID:SCR_006054

Type: Tool

Proper Citation

InterEvol database (RRID:SCR_006054)

Resource Information

URL: <http://biodev.cea.fr/interevol/>

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Description: InterEvol database is designed for the analysis of co-evolution events at the interface of known structures of hetero- and homo-oligomers. The database can be search and analyzed through 3 interconnected levels of analysis: * From a Keyword or the PDB entry of a complex, you can browse: ** structural homologs for every chain in other complexes ** structural interologs for every interface ** retrieve pre-computed sequence alignments in diverse species * From 1 or 2 sequences of interacting partners: ** build 2 multiple sequence alignments with the same species ordered in each ** query the InterEvol database with alignments using profile-profile comparison method * Visualize structure vs sequence alignment at the complex interface ** A dedicated Pymol plugin is provided ** Alignment views in Pymol are interactively restricted to the residues selected at the interface

Abbreviations: InterEvol

Resource Type: analysis service resource, data analysis service, data or information resource, database, production service resource, service resource, software resource

Defining Citation: [PMID:22053089](#)

Keywords: structure, evolution, protein complex, interface, protein complex, sequence alignment, plug in, protein structure, visualization, pymol plugin, structural homolog, structural interolog, bio.tools

Funding: Commissariat a l'Energie Atomique ;
ANR HPGenVar

Availability: Free and open to all users - no login requirement

Resource Name: InterEvol database

Resource ID: SCR_006054

Alternate IDs: nlx_151453, biotools:interevol

Alternate URLs: <https://bio.tools/interevol>

Record Creation Time: 20220129T080234+0000

Record Last Update: 20260821T193741+0000

Ratings and Alerts

No rating or validation information has been found for InterEvol database.

No alerts have been found for InterEvol database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

Marelli S, et al. (2020) Antagonism of PP2A is an independent and conserved function of HIV-1 Vif and causes cell cycle arrest. *eLife*, 9.

Bakail M, et al. (2019) Design on a Rational Basis of High-Affinity Peptides Inhibiting the Histone Chaperone ASF1. *Cell chemical biology*, 26(11), 1573.

Chen YQ, et al. (2018) Influenza Infection in Humans Induces Broadly Cross-Reactive and Protective Neuraminidase-Reactive Antibodies. *Cell*, 173(2), 417.

Caillet-Saguy C, et al. (2017) Regulation of the Human Phosphatase PTPN4 by the inter-domain linker connecting the PDZ and the phosphatase domains. *Scientific reports*, 7(1), 7875.

Launay G, et al. (2017) Non-interacting proteins may resemble interacting proteins: prevalence and implications. *Scientific reports*, 7, 40419.

Martin OM, et al. (2016) Implication of Terminal Residues at Protein-Protein and Protein-DNA Interfaces. *PloS one*, 11(9), e0162143.

Alsop JD, et al. (2015) Interolog interfaces in protein-protein docking. *Proteins*, 83(11), 1940.

Vasudevan HN, et al. (2014) SRF regulates craniofacial development through selective recruitment of MRTF cofactors by PDGF signaling. *Developmental cell*, 31(3), 332.

Hopf TA, et al. (2014) Sequence co-evolution gives 3D contacts and structures of protein complexes. *eLife*, 3.

Galperin MY, et al. (2012) The 2012 Nucleic Acids Research Database Issue and the online Molecular Biology Database Collection. *Nucleic acids research*, 40(Database issue), D1.